

SEQUENCE LISTING

<110> TOHOKU TECHNO ARCH CO., LTD.

<120> Novel Diabody-type Bispecific Antibody

<130> AB02035-US

<150> JP 2003-038643

<151> 2003-02-17

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<170> PatentIn version 3.1

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tca gtg aag ctg ccc tgc aag gct tct ggc gac aca ttc acc agt tac 96  
Ser Val Lys Leu Pro Cys Lys Ala Ser Gly Asp Thr Phe Thr Ser Tyr  
20 25 30  
tgg atg cac tgg gtg aag cag agg cat gga cat ggc cct gag tgg atc 144  
Trp Met His Trp Val Lys Gln Arg His Gly His Gly Pro Glu Trp Ile  
35 40 45  
gga aat att tat cca ggt agt ggt act aac tac gct gag aag ttc 192  
Gly Asn Ile Tyr Pro Gly Ser Gly Thr Asn Tyr Ala Glu Lys Phe  
50 55 60  
aag aac aag gtc act ctg act gta gac agg tcc tcc cgc aca gtc tac 240  
Lys Asn Lys Val Thr Leu Thr Val Asp Arg Ser Ser Arg Thr Val Tyr  
65 70 75 80  
atg cac ctc agc agg ctg aca tct gag gac tct gcg gtc tat tat tgt 288  
Met His Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
aca aga tcg ggg ggt ccc tac ttc ttt gac tac tgg ggc caa ggc acc 336  
Thr Arg Ser Gly Gly Pro Tyr Phe Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110  
act ctc aca gtc tcc tcc 354  
Thr Leu Thr Val Ser Ser  
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<222> (1)..(342)  
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gat caa gcc tcc atc tct tgc aga tct agt cag aac att gta cat aat 96  
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Asn  
20 25 30  
  
aat gga atc acc tat tta gaa tgg tac ctg caa agg cca ggc cag tct 144  
Asn Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Arg Pro Gly Gln Ser  
35 40 45  
  
cca aag ctc ctg atc tac aaa gtt tcc gac cga ttt tct ggg gtc cca 192  
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser Gly Val Pro  
50 55 60  
  
gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc 240  
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80  
  
agc aga gta gag gct gag gat ctg gga att tat tac tgc ttt caa ggt 288  
Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Phe Gln Gly  
85 90 95  
  
tca cat att cct ccc acg ttc gga ggg ggg acc aag ctg gaa atc aaa 336  
Ser His Ile Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
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<223> Chimeric Sequence (hOH)

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agc ctg cgc ctg tct tgc aaa gcg agc ggc tat acc ttt acg cgc tat 96  
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr  
20 25 30

acc atg cat tgg gtg cgc cag gcg ccg ggc aaa ggt ctg gaa tgg att 144  
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

ggc tat att aac ccg tct cgc ggc tat acc aac tat aat cag aaa gtg 192  
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val  
50 55 60

aaa gat cgc ttt acc att agc cgc gat aac tct aaa aac acc gcg ttt 240  
Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Ala Phe  
65 70 75 80

ctg cag atg gat agc ctg cgc ccg gaa gat acc ggc gtg tat ttt tgc 288  
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys  
85 90 95

gcg cgc tac tat gat gac cat tat agc ctg gat tat tgg ggc cag ggc 336  
Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly  
100 105 110

acc ccg gtg acc gtt agc tcg 357  
Thr Pro Val Thr Val Ser Ser  
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<211> 324

<212> DNA

<213> Artificial Sequence

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<222> (1)..(324)

<223> Chimeric Sequence (hOL)

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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gat	cgc	gtg	acc	att	acg	tgc	agc	gcf	tct	acg	tct	gtg	agc	tat	atg	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	
				20										30		
aac	tgg	tac	cag	caa	acc	cca	ggc	aaa	gcf	ccg	aaa	cgf	tgg	att	tat	144
Asn	Trp	Tyr	Gln	Gln	Thr	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile	Tyr	
				35										45		
gat	acc	agc	aaa	ctg	gcf	agc	ggc	gtg	ccg	agc	cgf	ttt	agc	ggc	tct	192
Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	
				50								60				
ggf	agc	ggc	acc	gat	tat	acg	ttt	acc	att	agc	tct	ctg	cag	ccg	gaa	240
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	
				65								75		80		
gat	att	gcf	acc	tat	tac	tgc	cag	caa	tgg	agc	tct	acc	ccg	ttt	acc	288
Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Phe	Thr	
				85								90		95		
ttt	ggc	cag	ggf	acc	aaa	ctg	cag	att	acc	ccg	gcf					324
Phe	Gly	Gln	Gly	Thr	Lys	Leu	Gln	Ile	Thr	Arg	Ala					
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Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1		5											10		15	
tcg	gtt	aaa	gtg	agc	tgc	aaa	gcc	tca	ggc	tat	acc	ttt	acg	agc	tac	96
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	
				20								25		30		
tgg	atg	cat	tgg	gtg	cgf	cag	gcc	ccg	ggf	cag	ggc	ctg	gaa	tgg	atg	144
Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
				35								40		45		

ggt aac att tat ccg ggc agc ggt ggc acc aac tat gcg gaa aaa ttt	192
Gly Asn Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Ala Glu Lys Phe	
50 55 60	
aag aac cgc gtg acc atg acg cgt gat acc agc att tcg acg gcc tat	240
Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr	
65 70 75 80	
atg gaa ctg agc cgc ctg cgt agc gat gac acc gcc gtg tat tac tgc	288
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg cgc agt ggc ggt ccg tat ttt ttc gat tac tgg ggc cag ggt acg	336
Ala Arg Ser Gly Gly Pro Tyr Phe Phe Asp Tyr Trp Gly Gln Gly Thr	
100 105 110	
ctg gtt acc gtg agc tcg	354
Leu Val Thr Val Ser Ser	
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gaa ccg gcg tcg att agc tgc cgc agc tcg cag aac atc gtg cat aat	96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Asn	
20 25 30	
aac ggc att acc tat ctg gaa tgg tat ctg cag aaa ccg ggc caa agc	144
Asn Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	
ccg cag ctg tta att tat aaa gtg agc gat cgc ttt agc ggc gtg ccg	192
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser Gly Val Pro	
50 55 60	
gat cgc ttt tcg ggc agc ggt agt ggc acc gat ttt acg ctg aaa att	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	

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agc cgc gtg gaa gcg gag gat gtt ggc gtg tat tac tgc ttt cag ggc				288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly				
85	90	95		
agc cat atc ccg cca acc ttt ggc caa ggc acc aaa gtg gaa att aaa				336
Ser His Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys				
100	105	110		
cgc gcg				342
Arg Ala				